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Figure 2

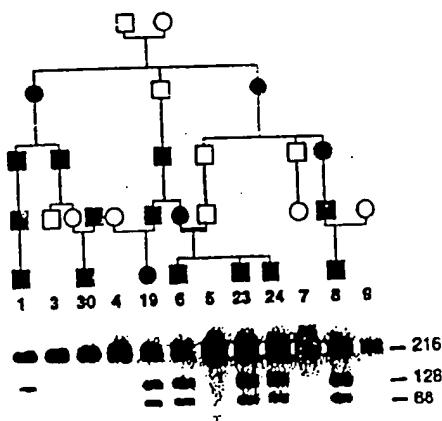
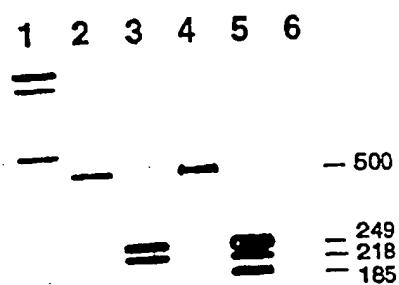


Figure 3

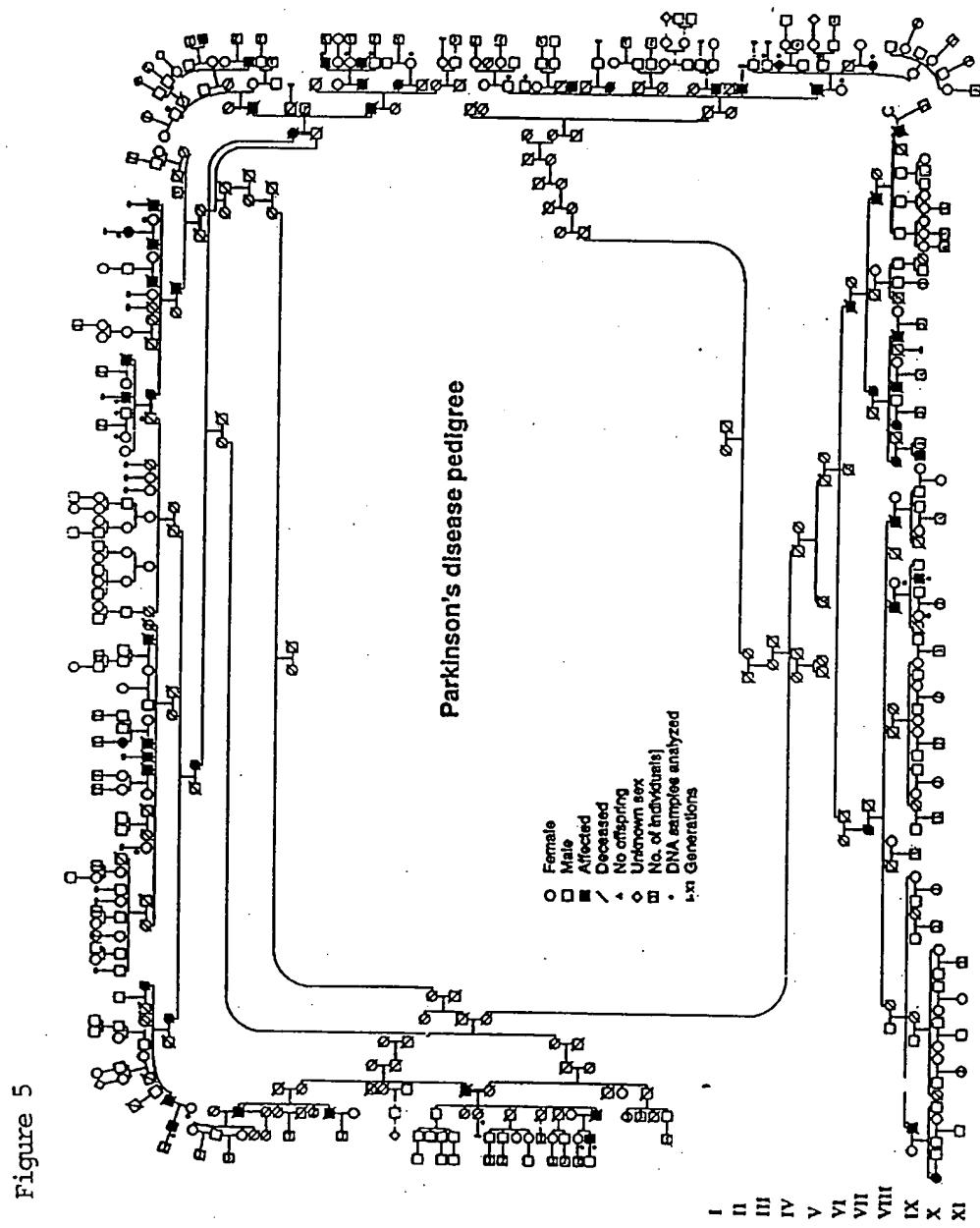


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Figure 4

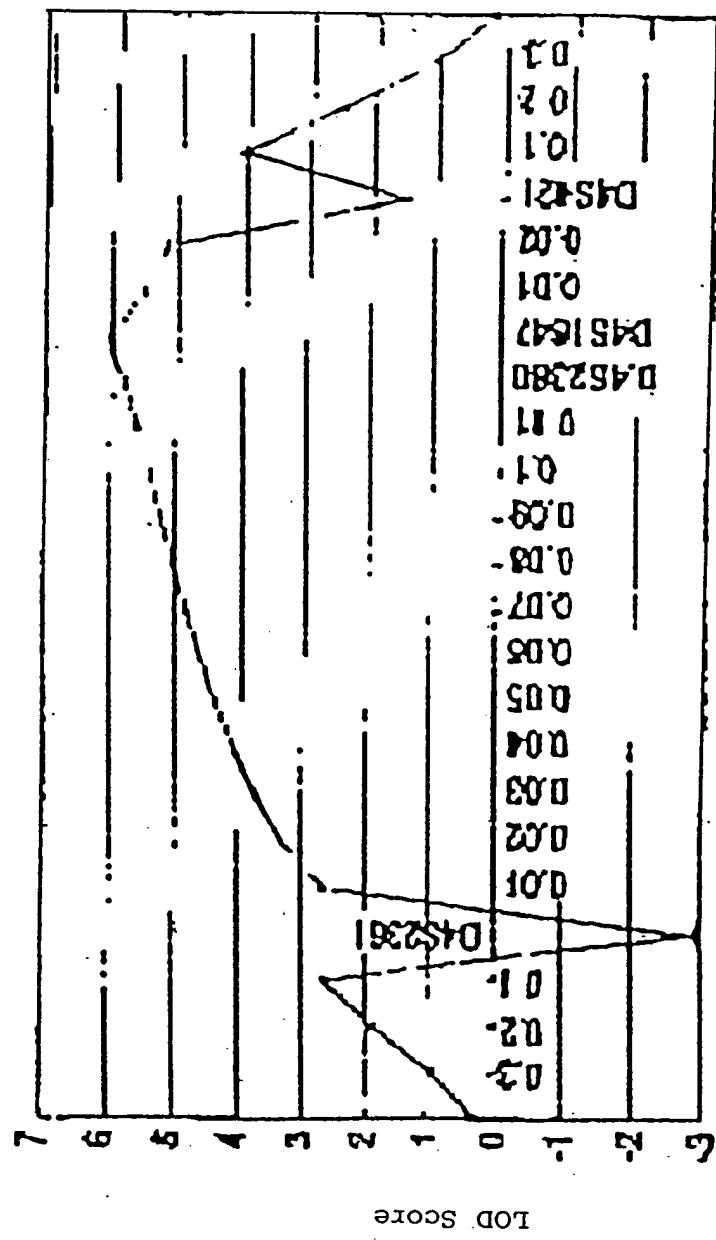
10	1	M D V F M K G L S K A K E G V V A A E K T K Q G V A E A A G K T - - - - -	20	1	M D V F M K G L S K A K E G V V A A E K T K Q G V A E A A G K T - - - - -	30	1	M D V F M K G L S M A K E G V V A A E K T K Q G V A E A A G K T - - - - -			
40	1	V G S K T K E G V V H G V @ A T V A E K T K E Q V T N V G A V V T G V T A V A Q K T V E G A G S I A	50	1	V G S K T K E G V V H G V T V A E K T K B Q V T N V G A V V T G V T A V A Q K T V E G A G N I A	60	1	V G S K T K E G V V H G V T V A E K T K E Q A S H L G G A V P S G A G - - - - -			
40	1	V G S K T K E G V V H G V T V A E K T K E Q V S N V G G A V V T G V T A V A Q K T V E G A G N I A	50	1	V G S R T K E G V V H G V T V A E K T K E Q V S V N T V T E K T K E Q V A G V N T V A S K T V E G V E N V A	60	1	V G T K T K E G V V H G V T V A E K T K E Q V A N V V G G A V V A G V N T V A S K T V E G V E N V A			
51	V	V G T K T K E G V V H G V T V A E K T K E Q V S V N T V T E K T K E Q V A N V V G G A V V A G V N T V A S K T V E G V E N V A	51	V	V G T K T K E G V V H G V T V A E K T K E Q V S V N T V T E K T K E Q V A N V V G G A V V A G V N T V A S K T V E G V E N V A	51	V	V G T K T K E G V V H G V T V A E K T K E Q V S V N T V T E K T K E Q V A N V V G G A V V A G V N T V A S K T V E G V E N V A			
90	1	A A T G F V K K D Q L G K - N - - E E G A P Q - - E G I - - L E D - - M P V D P D N E A Y E M P S	100	1	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S	110	1	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S	120	1	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S
90	A	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S	90	A	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S	90	A	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S	90	A	A A T G F V K K D Q M G K - G - - E E G Y P Q - - E G I - - L E D - - M P V D P S S E A Y E M P S
79	A	A A T G L V K K E E F P T - D L K P E E V A Q - - E A A E E P L I E - - P L M E P E G E S Y E E Q P	90	A	A A T G L V K K D Q L A K Q N - - E E 2 G F L Q - - E G M - - V N N T G A A V D P D N E A Y E M P P	101	A	A A T G L V K K D Q L A K Q N - - E E 2 G F L Q - - E G M - - V N N T G A A V D P D N E A Y E M P P	101	A	A A T G L V K K D Q L A K Q N - - E E 2 G F L Q - - E G M - - V N N T G A A V D P D N E A Y E M P P
130	A	A A S G V V K L D E H G R - E I P A E Q V A E B G K Q T T Q E P L V B - - A T E A T E - - - - -	130	A	A A S G V V K L D E H G R - E I P A E Q V A E B G K Q T T Q E P L V B - - A T E A T E - - - - -	130	A	A A S G V V K L D E H G R - E I P A E Q V A E B G K Q T T Q E P L V B - - A T E A T E - - - - -	130	A	A A S G V V K L D E H G R - E I P A E Q V A E B G K Q T T Q E P L V B - - A T E A T E - - - - -
130	E	E E G Y Q D D Y E P E A	130	E	E E G Y Q D D Y E P E A	130	E	E E G Y Q D D Y E P E A	130	E	E E G Y Q D D Y E P E A
124	Q	Q E E Y Q E Y E P E A	124	Q	Q E E Y Q E Y E P E A	124	Q	Q E E Y Q E Y E P E A	124	Q	Q E E Y Q E Y E P E A
133	E	E E E Y Q D D Y E P E A	133	E	E E E Y Q D D Y E P E A	133	E	E E E Y Q D D Y E P E A	133	E	E E E Y Q D D Y E P E A
140	-	- - - - -	140	-	- - - - -	140	-	- - - - -	140	-	- - - - -

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Figure 6



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Figure 7

clone	5'	3'	gene
109979	T84229	T88834	alpha
111088	T83410		alpha
111090	T83411	T81593	alpha
130048	R11619	(R18409)	alpha
135534	R31354	R32856	alpha
141248	R66863	R67383	alpha
145594	R78091	R77746	alpha
171906	H19290	H19291	beta
172284	H19556	H19474	beta
172749		H18685	beta
176546		H41126	beta
193174	H47503	H47504	alpha
210768	H66914	H66869	alpha
213616	H70324	H70325	alpha
236027	H62070		alpha
248153	N53829	N73325	alpha
24991	(T80528)	R39000	alpha
26298	R13508	(R20629)	alpha
265817	N28661	N21457	alpha
266628		N22757	alpha
27342		R37173	alpha
280344	(N50305)	N47094	alpha
290894		N72005	alpha
294142		N68597	alpha
307787	W21278		alpha
340635	W56712	W56757	alpha
340683	W55988	W56278	alpha
346647	W94390	W74638	alpha
346796	W79585	W79784	alpha
359349	AA010546	AA010547	alpha
364632	AA022809	AA022690	alpha
39915		R50455	beta
40764	R56327	R56245	alpha
45086	H08808	H08824	alpha
46607	H10267	H10213	alpha
49811	H29080	H28976	alpha
50202		H17962	beta
50470		H16811	beta
66473	R16018	R16119	alpha
687794	AA258686	AA258608	alpha
69907	T48654	T48655	alpha
72391	AA394097	AA293803	gamma
739009	AA421586		beta
739014	(AA42185)	AA421567	beta
771303		AA443638	gamma
2-4		L36675	alpha
2-5		L36674	alpha
c-01f06		F01363	alpha
c-1rb08	F03254	F06981	alpha
c-2td12	F08836	F11169	alpha
c-28f08	F03751	F07521	alpha
cDNA	S69965		beta
EST01420 (HRBAA27)	M78265		gamma
EST19193	AA317129		beta
EST22040	AA319774		alpha

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Figure 7 cont.

EST26845	T28079		beta
EST31489	AA328063		alpha
EST68G11	W22518		gamma
F1-625D	R29481		alpha
GEN-129D09	D81090		beta
hbc590	T11070		alpha
HIBBA65	T08213	T08212	alpha
	HR70E3R	HR70E3F	alpha
HSNACP0		U46896- 46901	alpha
KK1311	N83633		alpha
		D318839	alpha
		L08850	alpha
	T28735		alpha
	Z20502		alpha

Figure 8

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Figure 9

10 20 30 40

AGGGAGATCCAGCTCCGTCTGCCTGCAGCAGCACAAACCC 40
TGCACACCCACCATGGATGTCTTCAAGAAGGGCTTCTCCA 80
TCGCCAAGGAGGGXGTGGTGGGTGCGGTGGAAAAGACCAA 120
GCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGG 160
GTCATGTATGTGGGATTACATTTTTTTAAAGAAAGAA 200
210 220 230 240

TAAATTAAATTGTGATTAAGTTG 223

Figure 10

10 20 30 40

TTTTTTXAGGGGGAAAACAGGGAAATAAAXAXGGGG 40
GGGGGTTTTTXXGGGGGGGGGGGGAAAAXGGTTXGGGGX 80
XAACCXAAAXAAXXCCXAXGGGGGGGXAXXAAXTT 120
TGGGAACCCAAAGCCCXAGGAGGATTTTXGTXAAXAACG 160
TXACCTCXAGTGGXCGAGGAAGACCAAGGAAAXGCCAA 200
210 220 230 240

CXCAGTTGAXCGAGGCTGTGGTGAACAXCGTXAACXCTG 240
TCCCCXCCAAXAXCGTGGAGGXGGCGGAGAACATCSCGGT 280
CACCTCCGGGTGGTGCACAGGAGGACTTGAGGCCATCT 320
KCCCCCMAACAGGAGGGTGTGGCATCCMAAGARAAGAGG 360
AAGTGGCAGAGGAGGCCAGAGTGGGGGARACTAGAGGGC 400
410 420 430 440

TACAGGCCAGCGTGGATGACCTGAAGAGCGCTCCTCTGCC 440
TTGGACACCATCCCCCTCCTAGCACAAGGAGTGCCCCGCC 480
GAGTGACATGCGGCTGCCACGCTCCTGCCCTCGTCTTCC 520
TGGCCACCCCTGGCCTGTCCACCTGTGCTGCTGACCAAC 560
CTCACTGCCCTCCCTGGCCCCACCCACCCCTGGTCC 600
610 620 630 640

CTGACCCCACCTATGCTGCTGTGAATTTTTTTAAATG 640
ATTCCAAATAAAACTTGAGGCCACTCCAAAAAA 677

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Figure 11

alpha-SYN exons 1-2

10 20 30 40

AATTCAGCGATCGAGGGCAAAGCGCTCTCGGCGGTGCG 40
GTGTGAGCCACCTCCCAGCGCTGCCCTGTCTCCAGCAG 80
CTCCCCAAGGGATAAGGCTCTGCCCTGGTGGTCGACCCCTC 120
AGGCCCTCGNTCTCCAGGNCGACTCTGACGAGGGTAGG 160
GGGTGGTCCCCNGGAGGACCCAGAGGAAAGGCNGGGACAA 200

210 220 230 240

GAAGGGAGGGGAAGGGGAAAGAGGAAGAGGGCATCATCCCT 240
AGCCCAACCGCTCCCAGTCTCCACAAAGAGTGTGCGTGCAC 280
CTAAACTTAACGTGAGGCGCAAAAGCGCCCCAACCTTTTC 320
CCGCCTTGNNCCAGGCAGGCAGGCGGCTGGAGTTGATGGCTCAC 360
CCCGCGCCCCCTGCCCATCCCCATCCGAGATAGGGACGA 400

410 420 430 440

GGAGCACGCTGCAGGGAAAGCAGCGAGCGCCGGAGAGGG 440
GCAGGGCAGAACCGCTGACAAATCAGCGGTGGGGCGGAGA 480
GCCGAGGAGAAGGAGAAGGGAGGAGGACTAGGAGGAGGAGG 520
ACGGCGACGACCAAGAGGGCCCAAGAGAGGGGGCGAGCG 560
ACCGAGCGCCGCGACGCGAAGTGAGGTGCGTGCCTGGGCTCA 600

610 620 630 640

GCGCAGACCCCCGGCCCCCTCCCTGAGACGCTCTGGG 640
CGCTCCCTCACGCCCTTGCCCTCAAGCCTTCTGCCTTCCA 680
CCCTCGTGAGCGGAGAACTGGGAGTGGCCATTGACGACA 720
GGTTAGCGGGTTTGCCCTCCACTCCCCAGCCTCGCGTCG 760
CCGGCTCACAGCGGCCCTCCTCTGGGGACAGTCCCCCGG 800

810 820 830 840

GTGCCCTCCGCCCTTCCGTGCCCTCTTCTTC 840
TTTCCCTATTAAATATTATTGGAAATTGTTAAATTTC 880
TTTAAAAAAAGAGAGAGGGCGNGGAGGAGTCGGAGTTGTG 920
GAGAACGAGAGGACTCAGGTAAGTACCTGTGGATCTAAA 960
CGGGNGTCTTGGAAATCCTGGAGAACGCCGGATGGAGAC 1000

1010 1020 1030 1040

GAATGGTCGTGGNACCGGGAGGGGTGGTGCCTGCCATGA 1040
GGACCGCTGGGCCAGGTCTCTGGGAGGTGAGTACTTGTCC 1080
TTTGGGGAGCCTAAGGAAAGAGACTTGACCTGGCTTCGT 1120
CCTGCTTCTGATATTCCCTCTCCACAAGGGCTGAGAGNT 1160
TAGGCTGCTTCTCCGGGATCC 1181

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Figure 11 cont.

alpha-SYN exon 3

10 20 30 40
CTTAAAAGAGTCTCACACTTGGAGGGTTCTCATGATT 40
TTCAGTGTGTTTGTGTTATTTTCCCAGAAGTTCTCATT 80
CAAAGTGTATTTATGTTTCCAGTGTGGTGTAAAGAAAT 120
TCATTAGCCATGGATGTATTATGAAAGGACTTCAAAGG 160
CCAAGGAGGGAGTTGTGGCTGCTGAGAAAAACCAACA 200
210 220 230 240
GGGTGTGGCAGAACGAGCAGGAAAGACAAAAGAGGGTGT 240
CTCTATGTAGGTAGGTAACCCCCAAATGTCAGTTGGTGC 280
TTGTTCATGAGTGATGGGTTAGGATAACAATACTCTAAAT 320
GCTGGTAGTTCTCTCTTGATTCAATTGTCATCATTGC 360
TTGTCAAAAGGTGGACTGAGTCAGAGGTATGTGTAGGTA 400
410 420 430 440
GGTGAATGTGAACGTGTGATNTGAGCTAATAGTAAAAAT 440
GCGACTGTTGCTTTCAAGATTTAATTGGCTAATAT 480
NTATGACTNTTAAATGAATGTTCTGTACTACATAATT 520
CTATNTCAGAGACAGT 536

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Figure 11 cont.

alpha-SYN exon 4

10 20 30 40
CTGCAGGTCAACGGATCTGTCCTAGTGCTGTACTTTAA 40
AGCTTCTACAGTTCTGAATTCAAAATTATCTTCTCACTGG 80
GCCCGGTGTTATCTCATTCTTTCTCCTCTGTAAGTT 120
GACATGTGATGTGGAAACAAAGGGGATAAAAGTCATTATT 160
TGTGCTAAATCGTAATTGGAGAGGACCTCCTGTTAGCTG 200
210 220 230 240
GGCTTTCTTCTATNTATTGGGTGGTTAGGAGTTCTTCT 240
TCTAGTTTAGGATATATATATATATTTTTCTTCCCT 280
GAAGATATAATAATATATACTTCTGAAGATTGAGATT 320
TTAAATTAGTTGATTGAAAACTAGCTAATCAGCAATT 360
AGGCTAGCTTGAGACTTATGTCTGAATTGTTTAG 400
410 420 430 440
GCTCCAAAACCAAGGAGGGAGTGGTGCACTGGGTGGCAAC 440
AGGTAAGCTCCATTGTGCTTATATCAAAGATGATNTAA 480
AGTATCTAGTGTATTAGTGTGGCCCAGTATCAAGATTCTA 520
TGAAATTGTAACAAATCACTGAGCATCTAAGAACATATC 560
AGTCTTATTGAAACTGAATTCTTATAAAGTATTTTAA 600
610 620 630 640
TAGGTAATATTGATTATAAATAAAAAAATACTTGCCAA 640
GAATAATGAG 650

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Figure 11 cont.

alpha-SYN exon 5

10 20 30 40
ATATCTTAGCCAAGATTCAATGTTGGTTGAACCACACTC 40
ACTTGACATCTTGGTGGCTTTGTTCTTCTGACCACTCA 80
GTTATCTATGGCATGTGTAGATACAGGTGTATGGAANCAGA 120
TGGCTAGTGGAAAGTGGAAATGATTTAAGTCACTGTTATTTC 160
TACCAACCCCTTAAATCTGTTGCTCTTATTGTACCCAG 200
210 220 230 240
TGGCTGAGAAGACCAAAGAGCAAGTGACAAATGTTGGAGG 240
AGCAGTGGTGACGGGTGTGACAGCAGTAGCCAGAAGACA 280
GTGGAGGGAGCAGGGAGCATTGCAAGCAGCCACTGGCTTG 320
TCAAAAAGGACCAAGTTGGGCAAGGTATGGCTGTACGTT 360
TTGTGTTACATTATAAGCTGGTGAGATTACGGTTCAATT 400
410 420 430 440
TCATGTGAAGCCTGGAGGCAGGGAGCAAGATACTTACTGTG 440
GGGAACGGCTACCTGACCCCTCCCTGTGAAAAAGTGCTA 480
CCTTTATATTGGTCTTGCTTGT 504

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Figure 11 cont.

alpha-SYN exon 6

10 20 30 40
AAAAGTTACATACTTTGAGGTTGATAACCCATGTTGCCG 40
CAATGTTCCCCGGAGGCATTGTGGAGTTAGAATGCCAG 80
TAGTAATATTAAGGTGTGCCATTTCAGATCCGTGGCCA 120
ACATCCCTATATGTAAGATTTTCCAAAACATGGTTCTGA 160
TTTTAAAAGTAAAAATGCTACTTCATCATGTTTTTT 200
210 220 230 240
GTGCTTCTTACTTTAAATATTAGAATGAAGAAGGAGCCCC 240
ACAGGAAGGAATTCTGGAAGATATGCCTGTGGATCCTGAC 280
AATGAGGCTTATGAAATGCCTCTGAGGTAGGAGTCAAG 320
CTGAATCTTCTAACAAAGACAGTACCAAAACCTGTCATT 360
GTCACATTTCTTTCAATTAGTGCTTAGTGAGAACATCATT 400
410 420 430 440
GCTCTACATGCTCATTACGTGGACAACTTGCAAGTTAA 440
GAATAGTTTACATTTAAAGGGCTTAAAAAAAAG 480
AGGAGGAGGAAGATGAAGAAGAGGAAGAAAGGATGAAAA 520
GAAATCATATGTAGTCCACATAGCTTAATATACNTACTAC 560
TTGACCCCTTACAGGAAAGCTTACTAACCCCTGCATTA 600
610 620 630 640
GAGAATATATTTTGCAAAACATTGATTGAAATT 640
AGTGTAAAGTGGGGAGCCATTCTATCTCATTGGCTGTC 680
CAGTGCTGATGCGTAATTGAAACTTATACTAACAGTGTGT 720
GCTGTCT 727

Figure 11 cont.

alpha-SYN exon 7

10 20 30 40

TTTGATTTCTAATATTAGGAAGGGTATCAAGACTACG 40
 AACCTGAAGCCTAAGAAATATCTTGCTCCAGTTCTTG 80
 AGATCTGCTGACAGATGTTCCATCCTGTACAAGTGCTAG 120
 TTCCAATGTGCCAGTCATGACATTCTCAAAGTTTAC 160
 AGTGTATCTGAAGTCTTCATCAGCAGTGATTGAAGCAT 200

210 220 230 240

CTGTACCTGCCCACTCAGCATTGCGTGTCCCTTC 240
 ACTGAAGTGAATAACATGGTAGCAGGGTCTTGTGTGCTGT 280
 GGATTTGTGGCTTCATCTACGATGTTAAAACAAATTAA 320
 AAACACCTAAGTGAATCACCACCTATTCTAAATCCTCACT 360
 ATTTTTGTTGCTGTTAGAAGTTGTTAGTGATTG 400

410 420 430 440

CTATCATATATTATNAGATTTAGGTGTCTTTAATGAT 440
 ACTGTCTAAGAATAATGACGTATTGTGAAATTGTTAATA 480
 TATATNATACTAAAAATATGTGAGCATGAAACTATGCAC 520
 CTATAATACTAAATATGAAATTACCATTTGCGATGTG 560
 TTTTATTCACTGTGTTGTTATNAATGGTGAGAATTAA 600

610 620 630 640

AATAAAACGTTATCTCATTCGCAAAATATTTATTTTAT 640
 CCCATCTCACTTTAATAATAAAATCATGCTTATAAGCAA 680
 CATGAATAAGAACTGACACAAAGGACAAAATATAAGT 720
 TATTAATAGCCATTGAAGAAGGAGGAATTAGAAGAGG 760
 TAGAGAAAATGGAACATTAAACCTACACTCGGAATTCCCT 800

810 820 830 840

GAAGCAACACTGCCAGAAGTGTGTTGGTATGCACTGGT 840
 TCCTTAAGTGGCTGTGATTAATTATTGAAAGTGGGTGTT 880
 GAAGACCCCAACTACTATTGAGGTGGCTATTCTCCC 920
 TTCAATCCTGTCATGTTGCTTACGTATTTGGGGAAC 960
 TGTTGTTGATGTATGTGTTATAATTGTTACATT 1000

1010 1020 1030 1040

TTAATTGAGCCTTTATTAACATATATTGTTATTTTGTC 1040
 TCGAAATAATTGTTAGTTAAATCTATTGTCTGATAT 1080
 TGGTGTGAATGCTGTACCTTCTGACAATAAAATAATNC 1120
 GACCATGAATAAAAAAAAAAAAGTGGGTTCCCGGGAA 1160
 CTAAGCAGTGTAGAAGATGATTTGACTACACCCCTCTTA 1200

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Figure 11 cont.

alpha-SYN exon 7

1210 1220 1230 1240

GAGAGCCATAAGACACATTAGCACATATTAGCACATTCAA 1240
GGCTCTGAGAGAAATGTGGTTAACCTTGTTAACTCAGCAT 1280
TCCTCACTTTTTTTTTAATCATCAGAAATTCTCTCTCT 1320
CTCTCTCTTTCTCTCGCTCTTTTTTTTTTTTT 1360
TTTACAGGAAATGCCTTAAACATCGTTGGGAACATACCA 1400

1410 1420 1430 1440

GAGTCACCTTAAAGGGAGNATCAATTCTCTAGGACTGGAT 1440
AAAAATTTCATGGGCCTCTTAAATGTTGCCAAATAT 1480
ATGGAATTCTAGGGGTTTCCNTAGGGGGAAAGGGTTTT 1520
TCTCTTTCNGGGGAGGATCCTTAAACNCNNNGGGGG 1560
NGCCCGAAAATAAACTTGGNGGGGGGNAAAACCTT 1596